



SEQUENCE LISTING

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Zelinski, Thomas
Hauer, Bernhard

<120> L-RHAMNOSE-INDUCIBLE EXPRESSION SYSTEMS

<130> 12810-00091-US

<150> PCT/EP2003/013367
<151> 2003-11-27

<150> DE 102 56 381.0
<151> 2002-12-02

<160> 24

<170> PatentIn version 3.3

<210> 1
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<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (288)..(1121)
<223> coding for rhaS (positive regulator of rhaBAD operon)

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<222> (1108)..(2043)
<223> coding for rhaR (positive regulator of rhaRS operon)

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<222> (56)..(72)
<223> potential RhaS binding site

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<222> (89)..(105)
<223> potential RhaS binding site

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<222> (172)..(203)
<223> potential RhaR binding site

<220>
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<222> (210)..(241)
<223> potential RhaR binding site

<220>
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<222> (24)
<223> potential start of transcription (complement)

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cacaatttgc  tgaattgtgg  tgatgtgatg  ctccaccgat  ttcctgaaaa  ttcacgctgt  180
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gattaa

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<210> 2

<211> 287

<212> DNA

<213> Escherichia coli

<220>

<221> promoter

<222> (1)..(287)

<223> rhaBAD promoter fragment containing rhaS and rhaR binding sites

<400> 2

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tcaggaaatg  cggtgagcat  cacatcacca  caattcagca  aattgtgaac  atcatcacgt  180
tcacttttcc  ctggttgcca  atggcccatt  ttccgtcgag  taacgagaag  gtcgcgaatt  240
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287

<210> 3

<211> 125

<212> DNA

<213> Escherichia coli

<220>

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<221> promoter
<222> (1)..(125)
<223> rhaBAD promoter fragment containing RhaS binding site

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acgagaaggt cgcgaattca ggcgcttttt agactggtcg taatgaaatt cagcaggatc 120
acatt 125

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<211> 123
<212> DNA
<213> Escherichia coli

<220>
<221> promoter
<222> (1)..(123)
<223> rhaBAD promoter fragment containing RhaS binding site

<400> 4
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gcccathttc ctgtcagtaa cgagaaggtc gcgaattcag gcgcttttta gactggtcgt 120
aat 123

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<211> 51
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)..(51)
<223> palindromic RhaS binding site of rhaBAD promoter

<400> 5
atctttccct ggttgccaat ggcccathtt cctgtcagta acgagaaggt c 51

<210> 6
<211> 1071
<212> DNA
<213> Alcaligenes faecalis

<220>
<221> CDS
<222> (1)..(1068)
<223> coding for nitrilase

<400> 6
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Met Gln Thr Arg Lys Ile Val Arg Ala Ala Ala Val Gln Ala Ala Ser
1 5 10 15
ccc aac tac gat ctg gca acg ggt gtt gat aaa acc att gag ctg gct 96
Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala
20 25 30
cgt cag gcc cgc gat gag ggc tgt gac ctg atc gtg ttt ggt gaa acc 144
Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr
35 40 45
tgg ctg ccc gga tat ccc ttc cac gtc tgg ctg ggc gca ccg gcc tgg 192

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Trp	Leu	Pro	Gly	Tyr	Pro	Phe	His	Val	Trp	Leu	Gly	Ala	Pro	Ala	Trp	
50						55					60					
tcg	ctg	aaa	tac	agt	gcc	cgc	tac	tat	gcc	aac	tcg	ctc	tcg	ctg	gac	240
Ser	Leu	Lys	Tyr	Ser	Ala	Arg	Tyr	Tyr	Ala	Asn	Ser	Leu	Ser	Leu	Asp	
65					70					75					80	
agt	gca	gag	ttt	caa	cgc	att	gcc	cag	gcc	gca	cgg	acc	ttg	ggg	att	288
Ser	Ala	Glu	Phe	Gln	Arg	Ile	Ala	Gln	Ala	Ala	Arg	Thr	Leu	Gly	Ile	
				85						90					95	
ttc	atc	gca	ctg	ggg	tat	agc	gag	cgc	agc	ggc	ggc	agc	ctt	tac	ctg	336
Phe	Ile	Ala	Leu	Gly	Tyr	Ser	Glu	Arg	Ser	Gly	Gly	Ser	Leu	Tyr	Leu	
			100					105					110			
ggc	caa	tgc	ctg	atc	gac	gac	aag	ggc	gag	atg	ctg	tgg	tcg	cgt	cgc	384
Gly	Gln	Cys	Leu	Ile	Asp	Asp	Lys	Gly	Glu	Met	Leu	Trp	Ser	Arg	Arg	
		115				120						125				
aaa	ctc	aaa	ccc	acg	cat	gta	gag	cgc	acc	gta	ttt	ggg	gaa	ggg	tat	432
Lys	Leu	Lys	Pro	Thr	His	Val	Glu	Arg	Thr	Val	Phe	Gly	Glu	Gly	Tyr	
	130					135					140					
gcc	cgt	gat	ctg	att	gtg	tcc	gac	aca	gaa	ctg	gga	cgc	gtc	ggg	gct	480
Ala	Arg	Asp	Leu	Ile	Val	Ser	Asp	Thr	Glu	Leu	Gly	Arg	Val	Gly	Ala	
					150					155					160	
cta	tgc	tgc	tgg	gag	cat	ttg	tcg	ccc	ttg	agc	aag	tac	gcg	ctg	tac	528
Leu	Cys	Cys	Trp	Glu	His	Leu	Ser	Pro	Leu	Ser	Lys	Tyr	Ala	Leu	Tyr	
				165					170					175		
tcc	cag	cat	gaa	gcc	att	cac	att	gct	gcc	tgg	ccg	tcg	ttt	tcg	cta	576
Ser	Gln	His	Glu	Ala	Ile	His	Ile	Ala	Ala	Trp	Pro	Ser	Phe	Ser	Leu	
			180					185					190			
tac	agc	gaa	cag	gcc	cac	gcc	ctc	agt	gcc	aag	gtg	aac	atg	gct	gcc	624
Tyr	Ser	Glu	Gln	Ala	His	Ala	Leu	Ser	Ala	Lys	Val	Asn	Met	Ala	Ala	
			195				200					205				
tcg	caa	atc	tat	tcg	gtt	gaa	ggc	cag	tgc	ttt	acc	atc	gcc	gcc	agc	672
Ser	Gln	Ile	Tyr	Ser	Val	Glu	Gly	Gln	Cys	Phe	Thr	Ile	Ala	Ala	Ser	
			210			215					220					
agt	gtg	gtc	acc	caa	gag	acg	cta	gac	atg	ctg	gaa	gtg	ggg	gaa	cac	720
Ser	Val	Val	Thr	Gln	Glu	Thr	Leu	Asp	Met	Leu	Glu	Val	Gly	Glu	His	
				230						235					240	
aac	gcc	ccc	ttg	ctg	aaa	gtg	ggc	ggc	ggc	agg	tcc	atg	att	ttt	gcg	768
Asn	Ala	Pro	Leu	Leu	Lys	Val	Gly	Gly	Gly	Ser	Ser	Met	Ile	Phe	Ala	
				245					250					255		
ccg	gac	gga	cgc	aca	ctg	gct	ccc	tac	ctg	cct	cac	gat	gcc	gag	ggc	816
Pro	Asp	Gly	Arg	Thr	Leu	Ala	Pro	Tyr	Leu	Pro	His	Asp	Ala	Glu	Gly	
			260					265					270			
ttg	atc	att	gcc	gat	ctg	aat	atg	gag	gag	att	gcc	ttc	gcc	aaa	gcg	864
Leu	Ile	Ile	Ala	Asp	Leu	Asn	Met	Glu	Glu	Ile	Ala	Phe	Ala	Lys	Ala	
			275				280					285				
atc	aat	gac	ccc	gta	ggc	cac	tat	tcc	aaa	ccc	gag	gcc	acc	cgt	ctg	912
Ile	Asn	Asp	Pro	Val	Gly	His	Tyr	Ser	Lys	Pro	Glu	Ala	Thr	Arg	Leu	
			290			295					300					
gtg	ctg	gac	ttg	ggg	cac	cga	gac	ccc	atg	act	cgg	gtg	cac	tcc	aaa	960
Val	Leu	Asp	Leu	Gly	His	Arg	Asp	Pro	Met	Thr	Arg	Val	His	Ser	Lys	
				310						315					320	
agc	gtg	acc	agg	gaa	gag	gct	ccc	gag	caa	ggg	gtg	caa	agc	aag	att	1008
Ser	Val	Thr	Arg	Glu	Glu	Ala	Pro	Glu	Gln	Gly	Val	Gln	Ser	Lys	Ile	
				325					330					335		
gcc	tca	gtc	gct	atc	agc	cat	cca	cag	gac	tcg	gac	aca	ctg	cta	gtg	1056
Ala	Ser	Val	Ala	Ile	Ser	His	Pro	Gln	Asp	Ser	Asp	Thr	Leu	Leu	Val	
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caa	gag	ccg	tct	tga												1071
Gln	Glu	Pro	Ser													
		355														

<210> 7
 <211> 356
 <212> PRT
 <213> *Alcaligenes faecalis*

<400> 7
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 20 25 30
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 35 40 45
 Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp
 50 55 60
 Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp
 65 70 75 80
 Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile
 85 90 95
 Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu
 100 105 110
 Gly Gln Cys Leu Ile Asp Asp Lys Gly Glu Met Leu Trp Ser Arg Arg
 115 120 125
 Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Tyr
 130 135 140
 Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly Ala
 145 150 155 160
 Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu Tyr
 165 170 175
 Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu
 180 185 190
 Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala Ala
 195 200 205
 Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala Ser
 210 215 220
 Ser Val Val Thr Gln Glu Thr Leu Asp Met Leu Glu Val Gly Glu His
 225 230 235 240
 Asn Ala Pro Leu Leu Lys Val Gly Gly Gly Ser Ser Met Ile Phe Ala
 245 250 255
 Pro Asp Gly Arg Thr Leu Ala Pro Tyr Leu Pro His Asp Ala Glu Gly
 260 265 270
 Leu Ile Ile Ala Asp Leu Asn Met Glu Glu Ile Ala Phe Ala Lys Ala
 275 280 285
 Ile Asn Asp Pro Val Gly His Tyr Ser Lys Pro Glu Ala Thr Arg Leu
 290 295 300
 Val Leu Asp Leu Gly His Arg Asp Pro Met Thr Arg Val His Ser Lys
 305 310 315 320
 Ser Val Thr Arg Glu Glu Ala Pro Glu Gln Gly Val Gln Ser Lys Ile
 325 330 335
 Ala Ser Val Ala Ile Ser His Pro Gln Asp Ser Asp Thr Leu Leu Val
 340 345 350
 Gln Glu Pro Ser
 355

<210> 8
 <211> 1260
 <212> DNA
 <213> *Escherichia coli*

<220>
 <221> CDS

<222> (1)..(1257)

<223> coding for rhaA (L-rhamnose isomerase)

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1 5 10 15	
gcg gcg gtg ggg att gat gtc gag gag gcg ctg cgc caa ctt gat cgt	96
Ala Ala Val Gly Ile Asp Val Glu Glu Ala Leu Arg Gln Leu Asp Arg	
20 25 30	
tta ccc gtt tca atg cac tgc tgg cag ggc gat gat gtt tcc ggt ttt	144
Leu Pro Val Ser Met His Cys Trp Gln Gly Asp Asp Val Ser Gly Phe	
35 40 45	
gaa aac ccg gaa ggt tgc ctg acc ggg ggg att cag gcc aca ggc aat	192
Glu Asn Pro Glu Gly Ser Leu Thr Gly Gly Ile Gln Ala Thr Gly Asn	
50 55 60	
tat ccg ggc aaa gcg cgt aat gcc agt gag cta cgt gcc gat ctg gaa	240
Tyr Pro Gly Lys Ala Arg Asn Ala Ser Glu Leu Arg Ala Asp Leu Glu	
65 70 75 80	
cag gct atg cgg ctg att ccg ggg ccg aaa ccg ctt aat tta cat gcc	288
Gln Ala Met Arg Leu Ile Pro Gly Pro Lys Arg Leu Asn Leu His Ala	
85 90 95	
atc tat ctg gaa tca gat acg cca gtc tgc cgc gac cag atc aaa cca	336
Ile Tyr Leu Glu Ser Asp Thr Pro Val Ser Arg Asp Gln Ile Lys Pro	
100 105 110	
gag cac ttc aaa aac tgg gtt gaa tgg gcg aaa gcc aat cag ctc ggt	384
Glu His Phe Lys Asn Trp Val Glu Trp Ala Lys Ala Asn Gln Leu Gly	
115 120 125	
ctg gat ttt aac ccc tcc tgc ttt tgc cat ccg cta agc gcc gat ggc	432
Leu Asp Phe Asn Pro Ser Cys Phe Ser His Pro Leu Ser Ala Asp Gly	
130 135 140	
ttt acg ctt tcc cat gcc gac gac agc att cgc cag ttc tgg att gat	480
Phe Thr Leu Ser His Ala Asp Asp Ser Ile Arg Gln Phe Trp Ile Asp	
145 150 155 160	
cac tgc aaa gcc agc cgt cgc gtt tgc gcc tat ttt ggc gag caa ctc	528
His Cys Lys Ala Ser Arg Arg Val Ser Ala Tyr Phe Gly Glu Gln Leu	
165 170 175	
ggc aca cca tgc gtg atg aac atc tgg atc ccg gat ggt atg aaa gat	576
Gly Thr Pro Ser Val Met Asn Ile Trp Ile Pro Asp Gly Met Lys Asp	
180 185 190	
atc acc gtt gac cgt ctc gcc ccg cgt cag cgt ctg ctg gca gca ctg	624
Ile Thr Val Asp Arg Leu Ala Pro Arg Gln Arg Leu Leu Ala Ala Leu	
195 200 205	
gat gag gtg atc agc gag aag cta aac cct gcg cac cat atc gac gcc	672
Asp Glu Val Ile Ser Glu Lys Leu Asn Pro Ala His His Ile Asp Ala	
210 215 220	
gtt gag agc aaa ttg ttt ggc att ggc gca gag agc tac acg gtt ggc	720
Val Glu Ser Lys Leu Phe Gly Ile Gly Ala Glu Ser Tyr Thr Val Gly	
225 230 235 240	
tcc aat gag ttt tac atg ggg tat gcc acc agc cgc cag act gcg ctg	768
Ser Asn Glu Phe Tyr Met Gly Tyr Ala Thr Ser Arg Gln Thr Ala Leu	
245 250 255	
tgc ctg gac gcc ggg cac ttc cac ccg act gaa gtg att tcc gac aag	816
Cys Leu Asp Ala Gly His Phe His Pro Thr Glu Val Ile Ser Asp Lys	
260 265 270	
att tcc gcc gcc atg ctg tat gtg ccg cag ttg ctg ctg cac gtc agc	864
Ile Ser Ala Ala Met Leu Tyr Val Pro Gln Leu Leu Leu His Val Ser	
275 280 285	
cgt ccg gtt cgc tgg gac agc gat cac gta gtg ctg ctg gat gat gaa	912
Arg Pro Val Arg Trp Asp Ser Asp His Val Val Leu Leu Asp Asp Glu	
290 295 300	

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acc cag gca att gcc agt gag att gtg cgt cac gat ctg ttt gac cgg 960
Thr Gln Ala Ile Ala Ser Glu Ile Val Arg His Asp Leu Phe Asp Arg
305 310 315 320
gtg cat atc ggc ctt gac ttc ttc gat gcc tct atc aac cgc att gcc 1008
Val His Ile Gly Leu Asp Phe Phe Asp Ala Ser Ile Asn Arg Ile Ala
325 330 335
gcg tgg gtc att ggt aca cgc aat atg aaa aaa gcc ctg ctg cgt gcg 1056
Ala Trp Val Ile Gly Thr Arg Asn Met Lys Lys Ala Leu Leu Arg Ala
340 345 350
ttg ctg gaa cct acc gct gac gtg cgc aag ctg gaa gcg gcg ggc gat 1104
Leu Leu Glu Pro Thr Ala Asp Val Arg Lys Leu Glu Ala Ala Gly Asp
355 360 365
tac act gcg cgt ctg gca ctg ctg gaa gag cag aaa tcg ttg ccg tgg 1152
Tyr Thr Ala Arg Leu Ala Leu Glu Glu Gln Lys Ser Leu Pro Trp
370 375 380
cag gcg gtc tgg gaa atg tat tgc caa cgt cac gat acg cca gca ggt 1200
Gln Ala Val Trp Glu Met Tyr Cys Gln Arg His Asp Thr Pro Ala Gly
385 390 395 400
agc gaa tgg ctg gag agc gtg cgg gct tat gag aaa gaa att ttg agt 1248
Ser Glu Trp Leu Glu Ser Val Arg Ala Tyr Glu Lys Glu Ile Leu Ser
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cgc cgc ggg taa 1260
Arg Arg Gly

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<210> 9
<211> 419
<212> PRT
<213> Escherichia coli

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Leu Pro Val Ser Met His Cys Trp Gln Gly Asp Asp Val Ser Gly Phe
35 40 45
Glu Asn Pro Glu Gly Ser Leu Thr Gly Gly Ile Gln Ala Thr Gly Asn
50 55 60
Tyr Pro Gly Lys Ala Arg Asn Ala Ser Glu Leu Arg Ala Asp Leu Glu
65 70 75 80
Gln Ala Met Arg Leu Ile Pro Gly Pro Lys Arg Leu Asn Leu His Ala
85 90 95
Ile Tyr Leu Glu Ser Asp Thr Pro Val Ser Arg Asp Gln Ile Lys Pro
100 105 110
Glu His Phe Lys Asn Trp Val Glu Trp Ala Lys Ala Asn Gln Leu Gly
115 120 125
Leu Asp Phe Asn Pro Ser Cys Phe Ser His Pro Leu Ser Ala Asp Gly
130 135 140
Phe Thr Leu Ser His Ala Asp Asp Ser Ile Arg Gln Phe Trp Ile Asp
145 150 155 160
His Cys Lys Ala Ser Arg Arg Val Ser Ala Tyr Phe Gly Glu Gln Leu
165 170 175
Gly Thr Pro Ser Val Met Asn Ile Trp Ile Pro Asp Gly Met Lys Asp
180 185 190
Ile Thr Val Asp Arg Leu Ala Pro Arg Gln Arg Leu Leu Ala Ala Leu
195 200 205
Asp Glu Val Ile Ser Glu Lys Leu Asn Pro Ala His His Ile Asp Ala
210 215 220
Val Glu Ser Lys Leu Phe Gly Ile Gly Ala Glu Ser Tyr Thr Val Gly
225 230 235 240

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Ser Asn Glu Phe Tyr Met Gly Tyr Ala Thr Ser Arg Gln Thr Ala Leu
 245 250 255
 Cys Leu Asp Ala Gly His Phe His Pro Thr Glu Val Ile Ser Asp Lys
 260 265 270
 Ile Ser Ala Ala Met Leu Tyr Val Pro Gln Leu Leu Leu His Val Ser
 275 280 285
 Arg Pro Val Arg Trp Asp Ser Asp His Val Val Leu Leu Asp Asp Glu
 290 295 300
 Thr Gln Ala Ile Ala Ser Glu Ile Val Arg His Asp Leu Phe Asp Arg
 305 310 315 320
 Val His Ile Gly Leu Asp Phe Phe Asp Ala Ser Ile Asn Arg Ile Ala
 325 330 335
 Ala Trp Val Ile Gly Thr Arg Asn Met Lys Lys Ala Leu Leu Arg Ala
 340 345 350
 Leu Leu Glu Pro Thr Ala Asp Val Arg Lys Leu Glu Ala Ala Gly Asp
 355 360 365
 Tyr Thr Ala Arg Leu Ala Leu Leu Glu Glu Gln Lys Ser Leu Pro Trp
 370 375 380
 Gln Ala Val Trp Glu Met Tyr Cys Gln Arg His Asp Thr Pro Ala Gly
 385 390 395 400
 Ser Glu Trp Leu Glu Ser Val Arg Ala Tyr Glu Lys Glu Ile Leu Ser
 405 410 415
 Arg Arg Gly

<210> 10

<211> 1470

<212> DNA

<213> Escherichia coli

<220>

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<222> (1)..(1467)

<223> coding for rhaB (rhamnulokinase)

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 Met Thr Phe Arg Asn Cys Val Ala Val Asp Leu Gly Ala Ser Ser Gly
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 cgc gtg atg ctg gcg cgt tac gag cgt gaa tgc cgc agc ctg acg ctg 96
 Arg Val Met Leu Ala Arg Tyr Glu Arg Glu Cys Arg Ser Leu Thr Leu
 20 25 30
 cgc gaa atc cat cgt ttt aac aat ggg ctg cat agt cag aac ggc tat 144
 Arg Glu Ile His Arg Phe Asn Asn Gly Leu His Ser Gln Asn Gly Tyr
 35 40 45
 gtc acc tgg gat gtg gat agc ctt gaa agt gcc att cgc ctt gga tta 192
 Val Thr Trp Asp Val Asp Ser Leu Glu Ser Ala Ile Arg Leu Gly Leu
 50 55 60
 aac aag gtg tgc gag gaa ggg att cgt atc gat agc att ggg att gat 240
 Asn Lys Val Cys Glu Glu Gly Ile Arg Ile Asp Ser Ile Gly Ile Asp
 65 70 75 80
 acc tgg ggc gtg gac ttt gtg ctg ctc gac caa cag ggt cag cgt gtg 288
 Thr Trp Gly Val Asp Phe Val Leu Leu Asp Gln Gln Gly Gln Arg Val
 85 90 95
 ggc ctg ccc gtt gct tat cgc gat agc cgc acc aat ggc cta atg gcg 336
 Gly Leu Pro Val Ala Tyr Arg Asp Ser Arg Thr Asn Gly Leu Met Ala
 100 105 110
 cag gca caa caa caa ctc ggc aaa cgc gat att tat caa cgt agc ggc 384
 Gln Ala Gln Gln Leu Gly Lys Arg Asp Ile Tyr Gln Arg Ser Gly
 115 120 125
 atc cag ttt ctg ccc ttc aat acg ctt tat cag ttg cgt gcg ctg acg 432

Ile	Gln	Phe	Leu	Pro	Phe	Asn	Thr	Leu	Tyr	Gln	Leu	Arg	Ala	Leu	Thr	
130						135					140					
gag	caa	caa	cct	gaa	ctt	att	cca	cac	att	gct	cac	gct	ctg	ctg	atg	480
Glu	Gln	Gln	Pro	Glu	Leu	Ile	Pro	His	Ile	Ala	His	Ala	Leu	Leu	Met	
145					150					155					160	
ccg	gat	tac	ttc	agt	tat	cgc	ctg	acc	ggc	aag	atg	aac	tgg	gaa	tat	528
Pro	Asp	Tyr	Phe	Ser	Tyr	Arg	Leu	Thr	Gly	Lys	Met	Asn	Trp	Glu	Tyr	
				165					170					175		
acc	aac	gcc	acg	acc	acg	caa	ctg	gtc	aat	atc	aat	agc	gac	gac	tgg	576
Thr	Asn	Ala	Thr	Thr	Thr	Gln	Leu	Val	Asn	Ile	Asn	Ser	Asp	Asp	Trp	
			180					185					190			
gac	gag	tcg	cta	ctg	gcg	tgg	agc	ggg	gcc	aac	aaa	gcc	tgg	ttt	ggg	624
Asp	Glu	Ser	Leu	Leu	Ala	Trp	Ser	Gly	Ala	Asn	Lys	Ala	Trp	Phe	Gly	
		195					200					205				
cgc	ccg	acg	cat	ccg	ggg	aat	gtc	ata	ggg	cac	tgg	att	tgc	ccg	cag	672
Arg	Pro	Thr	His	Pro	Gly	Asn	Val	Ile	Gly	His	Trp	Ile	Cys	Pro	Gln	
	210				215						220					
ggg	aat	gag	att	cca	gtg	gtc	gcc	ggt	gcc	agc	cat	gat	acc	gcc	agc	720
Gly	Asn	Glu	Ile	Pro	Val	Val	Ala	Val	Ala	Ser	His	Asp	Thr	Ala	Ser	
225				230					235					240		
gcg	ggt	atc	gcc	tcg	ccg	tta	aac	ggc	tca	cgt	gct	gct	tat	ctc	tct	768
Ala	Val	Ile	Ala	Ser	Pro	Leu	Asn	Gly	Ser	Arg	Ala	Ala	Tyr	Leu	Ser	
				245				250						255		
tct	ggc	acc	tgg	tca	ttg	atg	ggc	ttc	gaa	agc	cag	acg	cca	ttt	acc	816
Ser	Gly	Thr	Trp	Ser	Leu	Met	Gly	Phe	Glu	Ser	Gln	Thr	Pro	Phe	Thr	
			260				265						270			
aat	gac	acg	gca	ctg	gca	gcc	aac	atc	acc	aat	gaa	ggc	ggg	gcg	gaa	864
Asn	Asp	Thr	Ala	Leu	Ala	Ala	Asn	Ile	Thr	Asn	Glu	Gly	Gly	Ala	Glu	
		275				280						285				
ggg	cgc	tat	cgg	gtg	ctg	aaa	aat	att	atg	ggc	tta	tgg	ctg	ctt	cag	912
Gly	Arg	Tyr	Arg	Val	Leu	Lys	Asn	Ile	Met	Gly	Leu	Trp	Leu	Leu	Gln	
	290				295					300						
cga	gtg	ctt	cag	gag	cag	caa	atc	aac	gat	ctt	ccg	gcg	ctt	atc	tcc	960
Arg	Val	Leu	Gln	Glu	Gln	Gln	Ile	Asn	Asp	Leu	Pro	Ala	Leu	Ile	Ser	
305				310						315					320	
gcg	aca	cag	gca	ctt	ccg	gct	tgc	cgc	ttc	att	atc	aat	ccc	aat	gac	1008
Ala	Thr	Gln	Ala	Leu	Pro	Ala	Cys	Arg	Phe	Ile	Ile	Asn	Pro	Asn	Asp	
			325					330					335			
gat	cgc	ttt	att	aat	cct	gag	acg	atg	tgc	agc	gaa	att	cag	gct	gcg	1056
Asp	Arg	Phe	Ile	Asn	Pro	Glu	Thr	Met	Cys	Ser	Glu	Ile	Gln	Ala	Ala	
		340					345						350			
tgt	cgg	gaa	acg	gcg	caa	ccg	atc	ccg	gaa	agt	gat	gct	gaa	ctg	gcg	1104
Cys	Arg	Glu	Thr	Ala	Gln	Pro	Ile	Pro	Glu	Ser	Asp	Ala	Glu	Leu	Ala	
		355				360						365				
cgc	tgc	att	ttc	gac	agt	ctg	gcg	ctg	ctg	tat	gcc	gat	gtg	ttg	cat	1152
Arg	Cys	Ile	Phe	Asp	Ser	Leu	Ala	Leu	Leu	Tyr	Ala	Asp	Val	Leu	His	
	370				375						380					
gag	ctg	gcg	cag	ctg	cgc	ggg	gaa	gat	ttc	tcg	caa	ctg	cat	att	gtc	1200
Glu	Leu	Ala	Gln	Leu	Arg	Gly	Glu	Asp	Phe	Ser	Gln	Leu	His	Ile	Val	
385				390						395				400		
ggc	gga	ggc	tgc	cag	aac	acg	ctg	ctc	aac	cag	cta	tgc	gcc	gat	gcc	1248
Gly	Gly	Gly	Cys	Gln	Asn	Thr	Leu	Leu	Asn	Gln	Leu	Cys	Ala	Asp	Ala	
			405					410					415			
tgc	ggg	att	cgg	gtg	atc	gcc	ggg	cct	ggt	gaa	gcc	tcg	acg	ctc	ggc	1296
Cys	Gly	Ile	Arg	Val	Ile	Ala	Gly	Pro	Val	Glu	Ala	Ser	Thr	Leu	Gly	
		420					425						430			
aat	atc	ggc	atc	cag	tta	atg	acg	ctg	gat	gaa	ctc	aac	aat	gtg	gat	1344
Asn	Ile	Gly	Ile	Gln	Leu	Met	Thr	Leu	Asp	Glu	Leu	Asn	Asn	Val	Asp	
		435				440						445				
gat	ttc	cgt	cag	gtc	gtc	agc	acc	acc	gcg	aat	ctg	acc	acc	ttt	acc	1392
Asp	Phe	Arg	Gln	Val	Val	Ser	Thr	Thr	Ala	Asn	Leu	Thr	Thr	Phe	Thr	

450		455		460	
cct aat cct gac agt gaa att gcc cac tat gtg gcg cag att cac tct					1440
Pro Asn Pro Asp Ser Glu Ile Ala His Tyr Val Ala Gln Ile His Ser					
465		470		475	480
aca cga cag aca aag gag ctt tgc gca tga					1470
Thr Arg Gln Thr Lys Glu Leu Cys Ala					
	485				

<210> 11
 <211> 489
 <212> PRT
 <213> Escherichia coli

<400> 11

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Arg	Val	Met	Leu	Ala	Arg	Tyr	Glu	Arg	Glu	Cys	Arg	Ser	Leu	Thr	Leu
			20					25					30		
Arg	Glu	Ile	His	Arg	Phe	Asn	Asn	Gly	Leu	His	Ser	Gln	Asn	Gly	Tyr
		35					40					45			
Val	Thr	Trp	Asp	Val	Asp	Ser	Leu	Glu	Ser	Ala	Ile	Arg	Leu	Gly	Leu
	50					55					60				
Asn	Lys	Val	Cys	Glu	Glu	Gly	Ile	Arg	Ile	Asp	Ser	Ile	Gly	Ile	Asp
65					70					75					80
Thr	Trp	Gly	Val	Asp	Phe	Val	Leu	Leu	Asp	Gln	Gln	Gly	Gln	Arg	Val
				85					90					95	
Gly	Leu	Pro	Val	Ala	Tyr	Arg	Asp	Ser	Arg	Thr	Asn	Gly	Leu	Met	Ala
			100					105					110		
Gln	Ala	Gln	Gln	Gln	Leu	Gly	Lys	Arg	Asp	Ile	Tyr	Gln	Arg	Ser	Gly
		115					120					125			
Ile	Gln	Phe	Leu	Pro	Phe	Asn	Thr	Leu	Tyr	Gln	Leu	Arg	Ala	Leu	Thr
	130					135					140				
Glu	Gln	Gln	Pro	Glu	Leu	Ile	Pro	His	Ile	Ala	His	Ala	Leu	Leu	Met
145					150					155					160
Pro	Asp	Tyr	Phe	Ser	Tyr	Arg	Leu	Thr	Gly	Lys	Met	Asn	Trp	Glu	Tyr
				165					170					175	
Thr	Asn	Ala	Thr	Thr	Thr	Gln	Leu	Val	Asn	Ile	Asn	Ser	Asp	Asp	Trp
			180					185					190		
Asp	Glu	Ser	Leu	Leu	Ala	Trp	Ser	Gly	Ala	Asn	Lys	Ala	Trp	Phe	Gly
		195					200					205			
Arg	Pro	Thr	His	Pro	Gly	Asn	Val	Ile	Gly	His	Trp	Ile	Cys	Pro	Gln
	210					215						220			
Gly	Asn	Glu	Ile	Pro	Val	Val	Ala	Val	Ala	Ser	His	Asp	Thr	Ala	Ser
225					230					235					240
Ala	Val	Ile	Ala	Ser	Pro	Leu	Asn	Gly	Ser	Arg	Ala	Ala	Tyr	Leu	Ser
				245						250				255	
Ser	Gly	Thr	Trp	Ser	Leu	Met	Gly	Phe	Glu	Ser	Gln	Thr	Pro	Phe	Thr
			260					265					270		
Asn	Asp	Thr	Ala	Leu	Ala	Ala	Asn	Ile	Thr	Asn	Glu	Gly	Gly	Ala	Glu
		275					280					285			
Gly	Arg	Tyr	Arg	Val	Leu	Lys	Asn	Ile	Met	Gly	Leu	Trp	Leu	Leu	Gln
	290					295					300				
Arg	Val	Leu	Gln	Glu	Gln	Gln	Ile	Asn	Asp	Leu	Pro	Ala	Leu	Ile	Ser
305					310					315					320
Ala	Thr	Gln	Ala	Leu	Pro	Ala	Cys	Arg	Phe	Ile	Ile	Asn	Pro	Asn	Asp
				325					330					335	
Asp	Arg	Phe	Ile	Asn	Pro	Glu	Thr	Met	Cys	Ser	Glu	Ile	Gln	Ala	Ala
			340					345					350		
Cys	Arg	Glu	Thr	Ala	Gln	Pro	Ile	Pro	Glu	Ser	Asp	Ala	Glu	Leu	Ala
		355					360					365			

Arg Cys Ile Phe Asp Ser Leu Ala Leu Leu Tyr Ala Asp Val Leu His
 370 375 380
 Glu Leu Ala Gln Leu Arg Gly Glu Asp Phe Ser Gln Leu His Ile Val
 385 390 395 400
 Gly Gly Gly Cys Gln Asn Thr Leu Leu Asn Gln Leu Cys Ala Asp Ala
 405 410 415
 Cys Gly Ile Arg Val Ile Ala Gly Pro Val Glu Ala Ser Thr Leu Gly
 420 425 430
 Asn Ile Gly Ile Gln Leu Met Thr Leu Asp Glu Leu Asn Asn Val Asp
 435 440 445
 Asp Phe Arg Gln Val Val Ser Thr Thr Ala Asn Leu Thr Thr Phe Thr
 450 455 460
 Pro Asn Pro Asp Ser Glu Ile Ala His Tyr Val Ala Gln Ile His Ser
 465 470 475 480
 Thr Arg Gln Thr Lys Glu Leu Cys Ala
 485

<210> 12
 <211> 825
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(822)
 <223> coding for rhaD (rhamnulose-phosphate aldolase)

<400> 12
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 Met Gln Asn Ile Thr Gln Ser Trp Phe Val Gln Gly Met Ile Lys Ala
 1 5 10 15
 acc acc gac gcc tgg ctg aaa ggc tgg gat gag cgc aac ggc gcc aac 96
 Thr Thr Asp Ala Trp Leu Lys Gly Trp Asp Glu Arg Asn Gly Gly Asn
 20 25 30
 ctg acg cta cgc ctg gat gac gcc gat atc gca cca tat cac gac aat 144
 Leu Thr Leu Arg Leu Asp Asp Ala Asp Ile Ala Pro Tyr His Asp Asn
 35 40 45
 ttc cac caa caa ccg cgc tat atc ccg ctc agc cag ccc atg cct tta 192
 Phe His Gln Gln Pro Arg Tyr Ile Pro Leu Ser Gln Pro Met Pro Leu
 50 55 60
 ctg gca aat aca ccg ttt att gtc acc ggc tcg ggc aaa ttc ttc cgt 240
 Leu Ala Asn Thr Pro Phe Ile Val Thr Gly Ser Gly Lys Phe Phe Arg
 65 70 75 80
 aac gtc cag ctt gat cct gcg gct aac tta ggc atc gta aaa gtc gac 288
 Asn Val Gln Leu Asp Pro Ala Ala Asn Leu Gly Ile Val Lys Val Asp
 85 90 95
 agc gac ggc gcg ggc tac cac att ctt tgg ggg tta acc aac gaa gcc 336
 Ser Asp Gly Ala Gly Tyr His Ile Leu Trp Gly Leu Thr Asn Glu Ala
 100 105 110
 gtc ccc act tcc gaa ctt ccg gct cac ttc ctt tcc cac tgc gag cgc 384
 Val Pro Thr Ser Glu Leu Pro Ala His Phe Leu Ser His Cys Glu Arg
 115 120 125
 att aaa gcc acc aac ggc aaa gat cgg gtg atc atg cac tgc cac gcc 432
 Ile Lys Ala Thr Asn Gly Lys Asp Arg Val Ile Met His Cys His Ala
 130 135 140
 acc aac ctg atc gcc ctc acc tat gta ctt gaa aac gac acc gcg gtc 480
 Thr Asn Leu Ile Ala Leu Thr Tyr Val Leu Glu Asn Asp Thr Ala Val
 145 150 155 160
 ttc act cgc caa ctg tgg gaa ggc agc acc gag tgt ctg gtg gta ttc 528
 Phe Thr Arg Gln Leu Trp Glu Gly Ser Thr Glu Cys Leu Val Val Phe

				165				170					175			
ccg	gat	ggc	gtt	ggc	att	ttg	ccg	tgg	atg	gtg	ccc	ggc	acg	gac	gaa	576
Pro	Asp	Gly	Val	Gly	Ile	Leu	Pro	Trp	Met	Val	Pro	Gly	Thr	Asp	Glu	
				180				185					190			
atc	ggc	cag	gcg	acc	gca	caa	gag	atg	caa	aaa	cat	tcg	ctg	gtg	ttg	624
Ile	Gly	Gln	Ala	Thr	Ala	Gln	Glu	Met	Gln	Lys	His	Ser	Leu	Val	Leu	
				195				200					205			
tgg	ccc	ttc	cac	ggc	gtc	ttc	ggc	agc	gga	ccg	acg	ctg	gat	gaa	acc	672
Trp	Pro	Phe	His	Gly	Val	Phe	Gly	Ser	Gly	Pro	Thr	Leu	Asp	Glu	Thr	
				210				215					220			
ttc	ggt	tta	atc	gac	acc	gca	gaa	aaa	tca	gca	caa	gta	tta	gtg	aag	720
Phe	Gly	Leu	Ile	Asp	Thr	Ala	Glu	Lys	Ser	Ala	Gln	Val	Leu	Val	Lys	
				225				230					235		240	
gtt	tat	tcg	atg	ggc	ggc	atg	aaa	cag	acc	atc	agc	cgt	gaa	gag	ttg	768
Val	Tyr	Ser	Met	Gly	Gly	Met	Lys	Gln	Thr	Ile	Ser	Arg	Glu	Glu	Leu	
				245				250					255			
ata	gcg	ctc	ggc	aag	cgt	ttc	ggc	gtt	acg	cca	ctc	gcc	agt	gcg	ctg	816
Ile	Ala	Leu	Gly	Lys	Arg	Phe	Gly	Val	Thr	Pro	Leu	Ala	Ser	Ala	Leu	
				260				265					270			
gcg	ctg	taa														825
Ala	Leu															

<210> 13

<211> 274

<212> PRT

<213> Escherichia coli

<400> 13

Met	Gln	Asn	Ile	Thr	Gln	Ser	Trp	Phe	Val	Gln	Gly	Met	Ile	Lys	Ala
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Thr	Thr	Asp	Ala	Trp	Leu	Lys	Gly	Trp	Asp	Glu	Arg	Asn	Gly	Gly	Asn
				20				25					30		
Leu	Thr	Leu	Arg	Leu	Asp	Asp	Ala	Asp	Ile	Ala	Pro	Tyr	His	Asp	Asn
				35			40					45			
Phe	His	Gln	Gln	Pro	Arg	Tyr	Ile	Pro	Leu	Ser	Gln	Pro	Met	Pro	Leu
				50			55				60				
Leu	Ala	Asn	Thr	Pro	Phe	Ile	Val	Thr	Gly	Ser	Gly	Lys	Phe	Phe	Arg
				65			70			75					80
Asn	Val	Gln	Leu	Asp	Pro	Ala	Ala	Asn	Leu	Gly	Ile	Val	Lys	Val	Asp
				85				90						95	
Ser	Asp	Gly	Ala	Gly	Tyr	His	Ile	Leu	Trp	Gly	Leu	Thr	Asn	Glu	Ala
			100					105					110		
Val	Pro	Thr	Ser	Glu	Leu	Pro	Ala	His	Phe	Leu	Ser	His	Cys	Glu	Arg
			115				120					125			
Ile	Lys	Ala	Thr	Asn	Gly	Lys	Asp	Arg	Val	Ile	Met	His	Cys	His	Ala
				130			135				140				
Thr	Asn	Leu	Ile	Ala	Leu	Thr	Tyr	Val	Leu	Glu	Asn	Asp	Thr	Ala	Val
				145			150			155					160
Phe	Thr	Arg	Gln	Leu	Trp	Glu	Gly	Ser	Thr	Glu	Cys	Leu	Val	Val	Phe
				165				170						175	
Pro	Asp	Gly	Val	Gly	Ile	Leu	Pro	Trp	Met	Val	Pro	Gly	Thr	Asp	Glu
			180					185					190		
Ile	Gly	Gln	Ala	Thr	Ala	Gln	Glu	Met	Gln	Lys	His	Ser	Leu	Val	Leu
			195				200					205			
Trp	Pro	Phe	His	Gly	Val	Phe	Gly	Ser	Gly	Pro	Thr	Leu	Asp	Glu	Thr
			210				215				220				
Phe	Gly	Leu	Ile	Asp	Thr	Ala	Glu	Lys	Ser	Ala	Gln	Val	Leu	Val	Lys
			225				230			235					240
Val	Tyr	Ser	Met	Gly	Gly	Met	Lys	Gln	Thr	Ile	Ser	Arg	Glu	Glu	Leu
				245				250						255	

Ile Ala Leu Gly Lys Arg Phe Gly Val Thr Pro Leu Ala Ser Ala Leu
 260 265 270
 Ala Leu

<210> 14
 <211> 939
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(936)
 <223> coding for rhaR (positive regulator for rhaRS operon)

<400> 14
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 Met Ala Phe Cys Asn Asn Ala Asn Leu Leu Asn Val Phe Val Arg His
 1 5 10 15
 att gcg aat aat caa ctt cgt tct ctg gcc gag gta gcc acg gtg gcg 96
 Ile Ala Asn Asn Gln Leu Arg Ser Leu Ala Glu Val Ala Thr Val Ala
 20 25 30
 cat cag tta aaa ctt ctc aaa gat gat ttt ttt gcc agc gac cag cag 144
 His Gln Leu Lys Leu Leu Lys Asp Asp Phe Phe Ala Ser Asp Gln Gln
 35 40 45
 gca gtc gct gtg gct gac cgt tat ccg caa gat gtc ttt gct gaa cat 192
 Ala Val Ala Val Ala Asp Arg Tyr Pro Gln Asp Val Phe Ala Glu His
 50 55 60
 aca cat gat ttt tgt gag ctg gtg att gtc tgg cgc ggt aat ggc ctg 240
 Thr His Asp Phe Cys Glu Leu Val Ile Val Trp Arg Gly Asn Gly Leu
 65 70 75 80
 cat gta ctc aac gat cgc cct tat cgc att acc cgt ggc gat ctc ttt 288
 His Val Leu Asn Asp Arg Pro Tyr Arg Ile Thr Arg Gly Asp Leu Phe
 85 90 95
 tac att cat gct gac gat aaa cac tcc tac gct tcc gtt aac gat ctg 336
 Tyr Ile His Ala Asp Asp Lys His Ser Tyr Ala Ser Val Asn Asp Leu
 100 105 110
 gtt ttg cag aat att att tat tgc ccg gag cgt ctg aag ctg aat ctt 384
 Val Leu Gln Asn Ile Ile Tyr Cys Pro Glu Arg Leu Lys Leu Asn Leu
 115 120 125
 gac tgg cag ggg gcg att ccg gga ttt aac gcc agc gca ggg caa cca 432
 Asp Trp Gln Gly Ala Ile Pro Gly Phe Asn Ala Ser Ala Gly Gln Pro
 130 135 140
 cac tgg cgc tta ggt agc atg ggg atg gcg cag gcg cgg cag gtt atc 480
 His Trp Arg Leu Gly Ser Met Gly Met Ala Gln Ala Arg Gln Val Ile
 145 150 155 160
 ggt cag ctt gag cat gaa agt agt cag cat gtg ccg ttt gct aac gaa 528
 Gly Gln Leu Glu His Glu Ser Ser Gln His Val Pro Phe Ala Asn Glu
 165 170 175
 atg gct gag ttg ctg ttc ggg cag ttg gtg atg ttg ctg aat cgc cat 576
 Met Ala Glu Leu Leu Phe Gly Gln Leu Val Met Leu Leu Asn Arg His
 180 185 190
 cgt tac acc agt gat tcg ttg ccg cca aca tcc agc gaa acg ttg ctg 624
 Arg Tyr Thr Ser Asp Ser Leu Pro Pro Thr Ser Ser Glu Thr Leu Leu
 195 200 205
 gat aag ctg att acc cgg ctg gcg gct agc ctg aaa agt ccc ttt gcg 672
 Asp Lys Leu Ile Thr Arg Leu Ala Ala Ser Leu Lys Ser Pro Phe Ala
 210 215 220
 ctg gat aaa ttt tgt gat gag gca tcg tgc agt gag cgc gtt ttg cgt 720
 Leu Asp Lys Phe Cys Asp Glu Ala Ser Cys Ser Glu Arg Val Leu Arg
 225 230 235 240

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cag caa ttt cgc cag cag act gga atg acc atc aat caa tat ctg cga 768
Gln Gln Phe Arg Gln Gln Thr Gly Met Thr Ile Asn Gln Tyr Leu Arg
245 250 255
cag gtc aga gtg tgt cat gcg caa tat ctt ctc cag cat agc cgc ctg 816
Gln Val Arg Val Cys His Ala Gln Tyr Leu Leu Gln His Ser Arg Leu
260 265 270
tta atc agt gat att tcg acc gaa tgt ggc ttt gaa gat agt aac tat 864
Leu Ile Ser Asp Ile Ser Thr Glu Cys Gly Phe Glu Asp Ser Asn Tyr
275 280 285
ttt tcg gtg gtg ttt acc cgg gaa acc ggg atg acg ccc agc cag tgg 912
Phe Ser Val Val Phe Thr Arg Glu Thr Gly Met Thr Pro Ser Gln Trp
290 295 300
cgt cat ctc aat tcg cag aaa gat taa 939
Arg His Leu Asn Ser Gln Lys Asp
305 310

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<210> 15
<211> 312
<212> PRT
<213> Escherichia coli

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20 25 30
His Gln Leu Lys Leu Leu Lys Asp Asp Phe Phe Ala Ser Asp Gln Gln
35 40 45
Ala Val Ala Val Ala Asp Arg Tyr Pro Gln Asp Val Phe Ala Glu His
50 55 60
Thr His Asp Phe Cys Glu Leu Val Ile Val Trp Arg Gly Asn Gly Leu
65 70 75 80
His Val Leu Asn Asp Arg Pro Tyr Arg Ile Thr Arg Gly Asp Leu Phe
85 90 95
Tyr Ile His Ala Asp Asp Lys His Ser Tyr Ala Ser Val Asn Asp Leu
100 105 110
Val Leu Gln Asn Ile Ile Tyr Cys Pro Glu Arg Leu Lys Leu Asn Leu
115 120 125
Asp Trp Gln Gly Ala Ile Pro Gly Phe Asn Ala Ser Ala Gly Gln Pro
130 135 140
His Trp Arg Leu Gly Ser Met Gly Met Ala Gln Ala Arg Gln Val Ile
145 150 155 160
Gly Gln Leu Glu His Glu Ser Ser Gln His Val Pro Phe Ala Asn Glu
165 170 175
Met Ala Glu Leu Leu Phe Gly Gln Leu Val Met Leu Leu Asn Arg His
180 185 190
Arg Tyr Thr Ser Asp Ser Leu Pro Pro Thr Ser Ser Glu Thr Leu Leu
195 200 205
Asp Lys Leu Ile Thr Arg Leu Ala Ala Ser Leu Lys Ser Pro Phe Ala
210 215 220
Leu Asp Lys Phe Cys Asp Glu Ala Ser Cys Ser Glu Arg Val Leu Arg
225 230 235 240
Gln Gln Phe Arg Gln Gln Thr Gly Met Thr Ile Asn Gln Tyr Leu Arg
245 250 255
Gln Val Arg Val Cys His Ala Gln Tyr Leu Leu Gln His Ser Arg Leu
260 265 270
Leu Ile Ser Asp Ile Ser Thr Glu Cys Gly Phe Glu Asp Ser Asn Tyr
275 280 285
Phe Ser Val Val Phe Thr Arg Glu Thr Gly Met Thr Pro Ser Gln Trp
290 295 300

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Arg His Leu Asn Ser Gln Lys Asp
305 310

<210> 16
<211> 837
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(834)
<223> coding for rhaS (positive regulator of rhaBAD operon)

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<400> 16
atg acc gta tta cat agt gtg gat ttt ttt ccg tct ggt aac gcg tcc 48
Met Thr Val Leu His Ser Val Asp Phe Phe Pro Ser Gly Asn Ala Ser
  1      5      10      15
gtg gcg ata gaa ccc cgg ctc ccg cag gcg gat ttt cct gaa cat cat 96
Val Ala Ile Glu Pro Arg Leu Pro Gln Ala Asp Phe Pro Glu His His
      20      25      30
cat gat ttt cat gaa att gtg att gtc gaa cat ggc acg ggt att cat 144
His Asp Phe His Glu Ile Val Ile Val Glu His Gly Thr Gly Ile His
      35      40      45
gtg ttt aat ggg cag ccc tat acc atc acc ggt ggc acg gtc tgt ttc 192
Val Phe Asn Gly Gln Pro Tyr Thr Ile Thr Gly Gly Thr Val Cys Phe
      50      55      60
gta cgc gat cat gat cgg cat ctg tat gaa cat acc gat aat ctg tgt 240
Val Arg Asp His Asp Arg His Leu Tyr Glu His Thr Asp Asn Leu Cys
      65      70      75      80
ctg acc aat gtg ctg tat cgc tcg ccg gat cga ttt cag ttt ctc gcc 288
Leu Thr Asn Val Leu Tyr Arg Ser Pro Asp Arg Phe Gln Phe Leu Ala
      85      90      95
ggg ctg aat cag ttg ctg cca caa gag ctg gat ggg cag tat ccg tct 336
Gly Leu Asn Gln Leu Leu Pro Gln Glu Leu Asp Gly Gln Tyr Pro Ser
      100      105      110
cac tgg cgc gtt aac cac agc gta ttg cag cag gtg cga cag ctg gtt 384
His Trp Arg Val Asn His Ser Val Leu Gln Gln Val Arg Gln Leu Val
      115      120      125
gca cag atg gaa cag cag gaa ggg gaa aat gat tta ccc tcg acc gcc 432
Ala Gln Met Glu Gln Gln Glu Gly Glu Asn Asp Leu Pro Ser Thr Ala
      130      135      140
agt cgc gag atc ttg ttt atg caa tta ctg ctc ttg ctg cgt aaa agc 480
Ser Arg Glu Ile Leu Phe Met Gln Leu Leu Leu Leu Leu Arg Lys Ser
      145      150      155      160
agt ttg cag gag aac ctg gaa aac agc gca tca cgt ctc aac ttg ctt 528
Ser Leu Gln Glu Asn Leu Glu Asn Ser Ala Ser Arg Leu Asn Leu Leu
      165      170      175
ctg gcc tgg ctg gag gac cat ttt gcc gat gag gtg aat tgg gat gcc 576
Leu Ala Trp Leu Glu Asp His Phe Ala Asp Glu Val Asn Trp Asp Ala
      180      185      190
gtg gcg gat caa ttt tct ctt tca ctg cgt acg cta cat cgg cag ctt 624
Val Ala Asp Gln Phe Ser Leu Ser Leu Arg Thr Leu His Arg Gln Leu
      195      200      205
aag cag caa acg gga ctg acg cct cag cga tac ctg aac cgc ctg cga 672
Lys Gln Gln Thr Gly Leu Thr Pro Gln Arg Tyr Leu Asn Arg Leu Arg
      210      215      220
ctg atg aaa gcc cga cat ctg cta cgc cac agc gag gcc agc gtt act 720
Leu Met Lys Ala Arg His Leu Leu Arg His Ser Glu Ala Ser Val Thr
      225      230      235      240
gac atc gcc tat cgc tgt gga ttc agc gac agt aac cac ttt tcg acg 768

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Asp Ile Ala Tyr Arg Cys Gly Phe Ser Asp Ser Asn His Phe Ser Thr
                245                250                255
ctt ttt cgc cga gag ttt aac tgg tca ccg cgt gat att cgc cag gga      816
Leu Phe Arg Arg Glu Phe Asn Trp Ser Pro Arg Asp Ile Arg Gln Gly
                260                265                270
cgg gat ggc ttt ctg caa taa
Arg Asp Gly Phe Leu Gln
                275

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837

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<210> 17
<211> 278
<212> PRT
<213> Escherichia coli

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<400> 17
Met Thr Val Leu His Ser Val Asp Phe Phe Pro Ser Gly Asn Ala Ser
  1          5          10          15
Val Ala Ile Glu Pro Arg Leu Pro Gln Ala Asp Phe Pro Glu His His
          20          25          30
His Asp Phe His Glu Ile Val Ile Val Glu His Gly Thr Gly Ile His
          35          40          45
Val Phe Asn Gly Gln Pro Tyr Thr Ile Thr Gly Gly Thr Val Cys Phe
          50          55          60
Val Arg Asp His Asp Arg His Leu Tyr Glu His Thr Asp Asn Leu Cys
          65          70          75          80
Leu Thr Asn Val Leu Tyr Arg Ser Pro Asp Arg Phe Gln Phe Leu Ala
          85          90          95
Gly Leu Asn Gln Leu Leu Pro Gln Glu Leu Asp Gly Gln Tyr Pro Ser
          100         105         110
His Trp Arg Val Asn His Ser Val Leu Gln Gln Val Arg Gln Leu Val
          115         120         125
Ala Gln Met Glu Gln Gln Glu Gly Glu Asn Asp Leu Pro Ser Thr Ala
          130         135         140
Ser Arg Glu Ile Leu Phe Met Gln Leu Leu Leu Leu Arg Lys Ser
          145         150         155         160
Ser Leu Gln Glu Asn Leu Glu Asn Ser Ala Ser Arg Leu Asn Leu Leu
          165         170         175
Leu Ala Trp Leu Glu Asp His Phe Ala Asp Glu Val Asn Trp Asp Ala
          180         185         190
Val Ala Asp Gln Phe Ser Leu Ser Leu Arg Thr Leu His Arg Gln Leu
          195         200         205
Lys Gln Gln Thr Gly Leu Thr Pro Gln Arg Tyr Leu Asn Arg Leu Arg
          210         215         220
Leu Met Lys Ala Arg His Leu Leu Arg His Ser Glu Ala Ser Val Thr
          225         230         235         240
Asp Ile Ala Tyr Arg Cys Gly Phe Ser Asp Ser Asn His Phe Ser Thr
          245         250         255
Leu Phe Arg Arg Glu Phe Asn Trp Ser Pro Arg Asp Ile Arg Gln Gly
          260         265         270
Arg Asp Gly Phe Leu Gln
          275

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<210> 18
<211> 1035
<212> DNA
<213> Escherichia coli

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<220>
<221> CDS

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<222> (1)..(1032)

<223> coding for rhaT (rhamnose transport protein)

<400> 18

atg agt aac gcg att acg atg ggg ata ttt tgg cat ttg atc ggc gcg	48
Met Ser Asn Ala Ile Thr Met Gly Ile Phe Trp His Leu Ile Gly Ala	
1 5 10 15	
gcc agt gca gcc tgt ttt tac gct ccg ttc aaa aaa gta aaa aaa tgg	96
Ala Ser Ala Ala Cys Phe Tyr Ala Pro Phe Lys Lys Val Lys Lys Trp	
20 25 30	
tca tgg gaa acc atg tgg tca gtc ggt ggg att gtt tcg tgg att att	144
Ser Trp Glu Thr Met Trp Ser Val Gly Gly Ile Val Ser Trp Ile Ile	
35 40 45	
ctg ccg tgg gcc atc agc gcc ctg tta cta ccg aat ttc tgg gcg tat	192
Leu Pro Trp Ala Ile Ser Ala Leu Leu Leu Pro Asn Phe Trp Ala Tyr	
50 55 60	
tac agc tcg ttt agt ctc tct acg cga ctg cct gtt ttt ctg ttc ggc	240
Tyr Ser Ser Phe Ser Leu Ser Thr Arg Leu Pro Val Phe Leu Phe Gly	
65 70 75 80	
gct atg tgg ggg atc ggt aat atc aac tac ggc ctg acc atg cgt tat	288
Ala Met Trp Gly Ile Gly Asn Ile Asn Tyr Gly Leu Thr Met Arg Tyr	
85 90 95	
ctc ggc atg tcg atg gga att ggc atc gcc att ggc att acg ttg att	336
Leu Gly Met Ser Met Gly Ile Gly Ile Ala Ile Gly Ile Thr Leu Ile	
100 105 110	
gtc ggt acg ctg atg acg cca att atc aac ggc aat ttc gat gtg ttg	384
Val Gly Thr Leu Met Thr Pro Ile Ile Asn Gly Asn Phe Asp Val Leu	
115 120 125	
att agc acc gaa ggc gga cgc atg acg ttg ctc ggc gtt ctg gtg gcg	432
Ile Ser Thr Glu Gly Gly Arg Met Thr Leu Leu Gly Val Leu Val Ala	
130 135 140	
ctg att ggc gta ggg att gta act cgc gcc ggg cag ttg aaa gag cgc	480
Leu Ile Gly Val Gly Ile Val Thr Arg Ala Gly Gln Leu Lys Glu Arg	
145 150 155 160	
aag atg ggc att aaa gcc gaa gag ttc aat ctg aaa aaa ggg ctg gtg	528
Lys Met Gly Ile Lys Ala Glu Glu Phe Asn Leu Lys Lys Gly Leu Val	
165 170 175	
ctg gcg gtg atg tgc ggc att ttc tct gcc ggg atg tcc ttt gcg atg	576
Leu Ala Val Met Cys Gly Ile Phe Ser Ala Gly Met Ser Phe Ala Met	
180 185 190	
aac gcc gca aaa ccg atg cat gaa gcc gct gcc gca ctt ggc gtc gat	624
Asn Ala Ala Lys Pro Met His Glu Ala Ala Ala Leu Gly Val Asp	
195 200 205	
cca ctg tat gtc gct ctg cca agc tat gtt gtc atc atg ggc ggc ggc	672
Pro Leu Tyr Val Ala Leu Pro Ser Tyr Val Val Ile Met Gly Gly Gly	
210 215 220	
gcg atc att aac ctc ggt ttc tgt ttt att cgt ctg gca aaa gtg aag	720
Ala Ile Ile Asn Leu Gly Phe Cys Phe Ile Arg Leu Ala Lys Val Lys	
225 230 235 240	
gat ttg tcg cta aaa gcc gac ttc tcg ctg gca aaa tcg ctg atc att	768
Asp Leu Ser Leu Lys Ala Asp Phe Ser Leu Ala Lys Ser Leu Ile Ile	
245 250 255	
cac aat gtg tta ctc tcg aca ctg ggc ggg ttg atg tgg tat ctg caa	816
His Asn Val Leu Leu Ser Thr Leu Gly Gly Leu Met Trp Tyr Leu Gln	
260 265 270	
ttc ttt ttc tat gcc tgg ggc cac gcc cgc att ccg gcg cag tat gac	864
Phe Phe Phe Tyr Ala Trp Gly His Ala Arg Ile Pro Ala Gln Tyr Asp	
275 280 285	
tac atc agt tgg atg ctg cat atg agt ttc tat gta ttg tgc ggc ggt	912
Tyr Ile Ser Trp Met Leu His Met Ser Phe Tyr Val Leu Cys Gly Gly	
290 295 300	

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atc gtc ggg ctg gtg ctg aaa gag tgg aac aat gca gga cgc cgt ccg 960
Ile Val Gly Leu Val Leu Lys Glu Trp Asn Asn Ala Gly Arg Arg Pro
305 310 315 320
gta acg gtg ttg agc ctc ggt tgt gtg gtg att att gtc gcc gct aac 1008
Val Thr Val Leu Ser Leu Gly Cys Val Val Ile Ile Val Ala Ala Asn
325 330 335
atc gtc ggc atc ggc atg gcg aat taa 1035
Ile Val Gly Ile Gly Met Ala Asn
340

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```

<210> 19
<211> 344
<212> PRT
<213> Escherichia coli

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<400> 19
Met Ser Asn Ala Ile Thr Met Gly Ile Phe Trp His Leu Ile Gly Ala
1 5 10 15
Ala Ser Ala Ala Cys Phe Tyr Ala Pro Phe Lys Lys Val Lys Lys Trp
20 25 30
Ser Trp Glu Thr Met Trp Ser Val Gly Gly Ile Val Ser Trp Ile Ile
35 40 45
Leu Pro Trp Ala Ile Ser Ala Leu Leu Leu Pro Asn Phe Trp Ala Tyr
50 55 60
Tyr Ser Ser Phe Ser Leu Ser Thr Arg Leu Pro Val Phe Leu Phe Gly
65 70 75 80
Ala Met Trp Gly Ile Gly Asn Ile Asn Tyr Gly Leu Thr Met Arg Tyr
85 90 95
Leu Gly Met Ser Met Gly Ile Gly Ile Ala Ile Gly Ile Thr Leu Ile
100 105 110
Val Gly Thr Leu Met Thr Pro Ile Ile Asn Gly Asn Phe Asp Val Leu
115 120 125
Ile Ser Thr Glu Gly Gly Arg Met Thr Leu Leu Gly Val Leu Val Ala
130 135 140
Leu Ile Gly Val Gly Ile Val Thr Arg Ala Gly Gln Leu Lys Glu Arg
145 150 155 160
Lys Met Gly Ile Lys Ala Glu Glu Phe Asn Leu Lys Lys Gly Leu Val
165 170 175
Leu Ala Val Met Cys Gly Ile Phe Ser Ala Gly Met Ser Phe Ala Met
180 185 190
Asn Ala Ala Lys Pro Met His Glu Ala Ala Ala Ala Leu Gly Val Asp
195 200 205
Pro Leu Tyr Val Ala Leu Pro Ser Tyr Val Val Ile Met Gly Gly Gly
210 215 220
Ala Ile Ile Asn Leu Gly Phe Cys Phe Ile Arg Leu Ala Lys Val Lys
225 230 235 240
Asp Leu Ser Leu Lys Ala Asp Phe Ser Leu Ala Lys Ser Leu Ile Ile
245 250 255
His Asn Val Leu Leu Ser Thr Leu Gly Leu Met Trp Tyr Leu Gln
260 265 270
Phe Phe Phe Tyr Ala Trp Gly His Ala Arg Ile Pro Ala Gln Tyr Asp
275 280 285
Tyr Ile Ser Trp Met Leu His Met Ser Phe Tyr Val Leu Cys Gly Gly
290 295 300
Ile Val Gly Leu Val Leu Lys Glu Trp Asn Asn Ala Gly Arg Arg Pro
305 310 315 320
Val Thr Val Leu Ser Leu Gly Cys Val Val Ile Ile Val Ala Ala Asn
325 330 335
Ile Val Gly Ile Gly Met Ala Asn
340

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<210> 20
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MKe258 Primer

<400> 20
 cccaagcttg gatcatgttt gctccttaca g 31

<210> 21
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MKe259 Primer

<400> 21
 gcgaattcgc atgaccactc aactggaaca 30

<210> 22
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MKe260 Primer

<400> 22
 cccaagctta ccgcgcgcga ctcaaaattt 30

<210> 23
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MKe001 Primer

<400> 23
 ataagaatgc ggccgcatga ccaactcaact ggaaca 36

<210> 24
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MKe002

<400> 24
 ctagctctag attacccgcg gcgactcaa 29